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OM protein - protein search, using sw model

Run on: May 30, 2002, 17:24:00 : Search time 11.84 seconds  
(without alignments)  
366,266 Million cell updates/sec

Title: US-09-730-617-4

Sequence: 1 MEGSLHFLAALACGYPLSM .....LSRPAYQIQYRLVQLQIK 112

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	535	94.2	121	1 NEMU_HUMAN	P08949 homo sapien
2	399	70.2	121	1 NEMU_MOUSE	Q06453 mus muscula
3	152	26.8	132	1 NEMU_HUMAN	P01297 sus scrofa
4	912	17.8	136	1 NEMU_HUMAN	P41851 ovis arien
5	95.5	16.2	136	1 GRP_SHEEP	P4443 xenopus lae
6	94	16.5	120	1 NEMU_XENLA	P24393 ratius norv
7	90.5	15.9	147	1 GRP_RAT	P23007 bomblin ori
8	83	14.6	155	1 GRP_BOMOR	P08947 phyllomedusa
9	79.5	14.0	90	1 LTRP_PHSXA	P21591 bomblin ori
10	77.5	13.6	119	1 BOMU_BOMOR	P21591 bomblin ori
11	73.5	13.1	90	1 LTRP_PHSXA	P21591 bomblin ori
12	71.5	12.6	4303	1 PRD1_HUMAN	P08161 homo sapien
13	70	12.3	107	1 BOMU_BOMOVA	P01296 bomblin var
14	70	12.3	339	1 PAX3_CHICK	P53166 gallus galli
15	69	12.1	145	1 RS23_YEAST	P32827 saccharomyc
16	67.5	11.9	695	1 PTD1_BOVIN	P10895 bos taurus
17	66.2	11.7	756	1 PTD1_PUTU	P30648 mycobacteri
18	66.2	11.7	756	1 PTD1_PUTU	P30648 mycobacteri
19	66.2	11.7	756	1 PTD1_PUTU	P30648 mycobacteri
20	66	11.6	82	1 RANA_KANPI	P08950 rana pipien
21	66	11.6	417	1 NTR2_MOUSE	P70310 mus musculu
22	65.5	11.5	1266	1 NGCA_CHICK	Q03696 gallus galli
23	65	11.4	155	1 BCP_JAEIN	P44411 haemophilus
24	64.5	11.4	327	1 YG29_STVY3	P7346 synechocyst
25	64.5	11.4	513	1 HEMU_HUMAN	P22830 homo sapien
26	64.5	11.4	513	1 HEMU_HUMAN	P22830 homo sapien
27	64.5	11.4	702	1 RPKA_BOVIN	Q06842 bovis tauri
28	64.5	11.4	1312	1 DPOL_PYSXD	Q51394 pyrococcus
29	64	11.3	143	1 RS23_SCHPO	P73057 schistosach
30	63.5	11.2	392	1 WNT1_BOMKO	P49340 bombyx mori
31	63.5	11.2	527	1 RAG2_MOUSE	P21784 mus musculu
32	63.5	11.2	639	1 NP72_SHEEP	Q97704 ovis aries
33	63.5	11.2	756	1 PTD1_HUMAN	P51176 homo sapien

34	63	11.1	261	1 KLU2_HUMAN	P20151 homo sapien
35	63	11.1	478	1 ERG_CHICK	Q06037 gallus galli
36	63	11.1	535	1 CTCL_MAZE	Q43250 zea mays (m
37	62.5	11.0	416	1 NTR2_RAT	Q63384 ratius norv
38	62.5	11.0	1536	1 Y327_HST11	Q57359 icterulid
39	62	10.9	1536	1 Y327_HST11	Q57359 icterulid
40	62	10.9	2453	1 NCRL_MOUSE	Q06924 mus musculu
41	61.5	10.8	1654	1 PCPR_HUMAN	Q09433 mus sapien
42	61.5	10.8	2236	1 PYR1_DROME	P05990 drosophila
43	61	10.7	502	1 SYFA_HUMAN	P15625 saccharomyc
44	61	10.7	554	1 YER2_YEAST	P40055 saccharomyc
45	60.5	10.7	227	1 ACIL1_DYCES	Q40170 lycopersico

## ALIGNMENTS

RESULT	1	STANDARD	PRT	121 AA.
NEBU_HUMAN				
1	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN
2	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN
3	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN
4	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN
5	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN
6	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN
7	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN
8	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN
9	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN
10	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN
11	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN
12	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN
13	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN
14	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN
15	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN
16	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN
17	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN
18	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN
19	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN
20	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN
21	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN
22	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN
23	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN
24	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN
25	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN
26	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN
27	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN
28	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN
29	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN
30	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN
31	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN
32	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN
33	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN
34	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN
35	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN
36	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN
37	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN
38	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN
39	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN
40	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN
41	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN
42	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN
43	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN
44	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN
45	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN	NEBU_HUMAN

Bombesin family; Amidation: Cleavage on pair of basic residues;  
 KW Signal: Alternative splicing.  
 FT Peptide 1 54 NEUROMEDIN B-32.  
 FT Peptide 2 56 NEUROMEDIN B.  
 FT PROPEP 47 56  
 FT MOD.RES 60 121  
 FT VARSPLIC 111 121  
 FT CONTRACT 68 76  
 FT SEQUENCE 121 AA, 13255 MM: LTRF001466031B CRC64.  
 Query Match 94.2% Score 395; DB 1; Length 121;  
 Best Local Similarity 95.5% Pred. No. 1.4e-50;  
 Matches 107; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 Oy 1 MEGSLIFALLAAGVPLSNOLPEPRASAKTIHYHNRKQNLAKIGHCKKSLSPSSSTPL 60  
 Db 10 MEGSLIFALLAAGVPLSNOLPEPRASAKTIHYHNRKQNLAKIGHCKKSLSPSSSTPL 69  
 Oy 61 GAPTPTSLRQRLQSLHDLGLILLKRAKAGVLSRPAPQIYQRLVLIQILK 112  
 Db 70 GAPTPTSLRQRLQSLHDLGLILLKRAKAGVLSRPAPQIYQRLVLIQILK 121  
 RESULT 2  
 NEUR\_MOUSE STANDARD PRT: 121 AA.  
 AC Q9GCR53;  
 DT 01-MAR-2002 (rel. 41, Created)  
 DT 01-MAR-2002 (rel. 41, Last sequence update)  
 DT 01-MAR-2002 (rel. 41, Last annotation update)  
 DE Neureomedin B-32 precursor (contains: Neureomedin B).  
 GN NMB  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 CX NCBI\_TaxID=10090;  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Embryonic head, and Embryo;  
 RA MEDLINE=1085660; PubMed=1217851;  
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Aizawa K., Iizawa H., Nishi K., Kiyosawa H., Kondo S., Yamakita I.,  
 RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,  
 RA Flothmann T., Gharifard T., Glasi C., Kiro B., Kocher H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikelid J., Pasole G., Quakenbush J.,  
 RA Schirral L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Blake J., Boffelli D., Bojunga N., Carfagna P., de Bonaldi M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Lyons M., Michon A., Nishida H., Hume D.A., Kamilya M., Lee N.H.,  
 RA Nordens P., Ring B., Ringwald M., Rodriguez L., Skokanov R.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilmink L.,  
 RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kozaki S.,  
 RA Hayashizaki Y.;  
 RA Functional annotation of a full-length mouse cDNA collection.\*;  
 RA Medline=93282813; PubMed=6862442;  
 RL Neureomedin B-32.  
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 CC -----  
 DR EMBL: AK014077; BAB29144.1; -;  
 DR EMBL: AK011929; BAB27922.1; -;  
 DR MIM: M011915289; Nmb.  
 DR InterPro: IPR000874; Bombesin.  
 DR Pfam: PF02044; Bombesin.1.  
 DR PROSITE: PS00257; BOMBESIN; 1.  
 CC Bombesin family; Amidation: Cleavage on pair of basic residues;  
 KW SIGNAL: BY SIMILARITY.  
 FT Peptide 1 24 NEUROMEDIN B-32.  
 FT Peptide 2 56 NEUROMEDIN B.  
 FT PROPEP 47 56  
 FT MOD.RES 60 121  
 FT CONTRACT 68 76  
 FT SEQUENCE 121 AA, 13571 MM: LTRF001466031B CRC64.  
 Query Match 70.2% Score 399; DB 1; Length 121;  
 Best Local Similarity 75.0% Pred. No. 5.3e-36;  
 Matches 81; Conservative 7; Mismatches 20; Indels 0; Gaps 0;  
 Oy 5 LTRFALLAAGVPLSNOLPEPRASAKTIHYHNRKQNLAKIGHCKKSLSPSSSTPL 64  
 Db 14 LTRFALLAAGVPLSNOLPEPRASAKTIHYHNRKQNLAKIGHCKKSLSPSSSTPL 73  
 Oy 65 FRTSLRQRLQSLHDLGLILLKRAKAGVLSRPAPQIYQRLVLIQILK 112  
 Db 74 FRTSLRQRLQSLHDLGLILLKRAKAGVLSRPAPQIYQRLVLIQILK 121  
 RESULT 3  
 NEUR\_PIG STANDARD PRT: 32 AA.  
 AC P01297;  
 DT 21-JUL-1986 (rel. 01, Created)  
 DT 01-NOV-1986 (rel. 09, Last sequence update)  
 DT 01-NOV-1986 (rel. 09, Last annotation update)  
 DE Neureomedin B-32 [contains: Neureomedin B].  
 GN NMB  
 OS Sus scrofa (Pig).  
 CC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.  
 CX NCBI\_TaxID=9823;  
 RN SEQUENCE  
 RA MEDLINE=85279454; PubMed=4026853;  
 RA Minamoto N., Sudoh T., Kanegawa K., Matsuo H.;  
 RT "Neureomedin B-32 and B-30: Two 'big' neureomedin B identified in  
 RT porcine brain and spinal cord.";  
 RL Biochem. Biophys. Res. Commun. 130:685-691(1985).  
 RN SEQUENCE  
 RA Minamoto N., Kanegawa K., Matsuo H.;  
 RT "Neureomedin B and neureomedin C: two mammalian bombesin-like peptides  
 RT identified in pig spinal cord and brain.";  
 RL Regul. Pept. 19:127-127(1987).  
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CC or send an email to licenses@isdb.sib.ch).
CC
DR EMBL; R02050.1; AA55261.1; -
DR EMBL; M1253.1; AA55611.1; -
DR EMBL; M1251.1; AA55611.1; JOINED.
DR EMBL; M1251.2; AA55611.1; JOINED.
DR EMBL; M1251.1; AA55611.1; JOINED.
DR EMBL; M1251.1; AA55611.1; JOINED.
DR EMBL; BC004488; AAB04488.1; -.
DR PIR; B26182; B26182.
DR PIR; A11200; A11200.
DR TrEMBL; F0900874; Bombesin.
DR TrEMBL; F0900874; Bombesin.
DR Pfam; PF02044; Bombesin_1.
DR ProSite; PS00257; BOMBESIN; 1.
KW Bombesin family; Amidation; Cleavage on pair of basic residues;
KW signal; Alternative splicing.
FT SIGNAL         1                23
FT PEPTIDE        24               50
FT PROPEP         44               50
FT MOD_RES        54              148
FT VARSPIC        122             148
FT VARSPLIC       128             134
FT CONFLICT        4               4
FT SEQUENCE       148 AA; 16144 MW; 2B55B9350A425466 CRC64;
FO
Query Match          17.2%   Score 97.5; DB 1; Length 148;
Best local similarity 3.5%; Pred. No. 0.0014;
Matches    40; Conservative 13; Mismatches 26; Indels 37; Gaps 7;
QY      1 MFSLIFALLAAAGVPLISMDLPERSRASKI-----RHNSRGKMAIGHFNGKRS 51
DB      1 HOSBRLPVYLAL-VLCIA-----FKHRYVLDAAGGTYATKRTPFGSHNVAHGHIIM 54
           ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY      53 L-PSSPSPTGAPHRHSVRROQL-----QMSDIDLLITLLK-----KALD 90
           ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      55 TGESSVSERG----SLKQOLREYRMELAEANILCLTEAKENRNHPPOPKALE 105
           ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
RESULT
GRP_SHEEP
ID GRP_SHEEP STANDARD; PROT; 134 AA.
AC P47651.
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Gastrin-releasing peptide precursor (GRP) [Contains: Neuremedin C
DP (-10)].
GN Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OX Bovidae; Caprinae; Ovis.
OX NCBI_Taxid=9940;
SEQUENCE FROM N.A.
MEDLINE#95080110. PubMed#7986429;
Praser M., McDonald T.J., Spindel E.R., Fahy M., Hill D.,
Challis J.R.;
"Gastrin-releasing peptide is produced in the pregnant ovine uterus."
Endocrinology 135:2440-2445(1994).
RT -1- FUNCTION: GRP stimulates gastrin release as well as other
CC functions.
CC -1- SUBCELLULAR LOCATION: secreted.
CC -1- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANNTENSIN
CC FAMILY.
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ID	BOMB_BOMOR	STANDARD:	PRT:	119 AA.
Dt	01-APR-1991 (rel. 18)			
Dt	01-MAY-1991 (rel. 19)			
Dt	01-MAY-1991 (rel. 18)			Last sequence update)
Dt	01-MAR-2002 (rel. 41)			Last annotation update)
Dt	Bombesin precursor.			
Oc	Bombina orientalis (Oriental fire-bellied toad).			
Oc	Eukaryota; Metazoa; Chordata; Cephalia; Vertebrata; Euteleostomi;			
Oc	Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.			
Ox	NCB1_taxid:89346;			
Rp	SEQUENCE FROM N.A.			
Rp	MEDLINE-91088602; PubMed-2263631;			
Rt	Splindel E.R., Gibson B.W., Reeve J.R. Jr., Kelly M.;			
Rt	Cloning of cDNA encoding amphibian bombesin: evidence for the			
Rt	relationship between bombesin and gastrin-releasing peptide.*			
Rl	Proc. Natl. Acad. Sci. U.S.A. 87:9813-9817(1990).			
Cc	-1- FUNCTION: ESTABLISHES SMOOTH MUSCLE CONTRACTION. ROLE IN INDUCTION			
Cc	GASTROINTESTINAL HORMONES OR DNA REPLICATION AND RELEASE OF MANY			
Cc	-1- TISSUE SPECIFICITY: LOCALIZED TO THE CUTANEOUS GRANULAR GLANDS IN			
Cc	THE SKIN AND THE BRAIN.			
Cc	-1- SIMILARITY: BELONGS TO THE BOMBESIN/NEUREGONIN B/RANNTENSIN			
Cc	FAMILY.			
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Cc	modified and this statement is not removed. Usage by and for commercial			
Cc	entities requires a license agreement (see http://www.isb-sib.ch/announce/			
Cc	or send an email to license@isb-sib.ch).			
Cc	EMBL; MS5255; AAAA5551.1; -			
Df	PIR; A39261; A39261.			
Df	InterPro; IPRO00874; Bombsen.			
Df	Pfam; PF02040; Bombsen; 1.			
Df	DR PROSITE; PS00237; BOMBESIN; 1.			
Kw	Bombesin family; Amidation; Cleavage on pair of basic residues:			
Kw	Signal.			
Ft	FM SIGNAL.			
Ft	PROPSP	1	29	POTENTIAL.
Ft	PEPTIDE	30	44	
Ft	PROPEP	42	58	BOMBESIN.
Ft	MOD_RES	58	58	
St	SEQUENCE	119 AA;	13863 MW;	3A3D84DA2445A44A CRC64;
Query Match		13.6%; Score 77.5;	DB 1;	Length 119;
Best Local Similarity		30.3%;		
Matches	23;	Conservative 13;	Mismatches 35;	Indels 5;
			Gaps 3;	
Oy	3 GSELRHALLAAVQVPYS-NMDEPRRSRRSRKIVISR-GMALVAIGFPGKKSLSPSSPP 59			
Db	13 GELRH--LLTFSSLSLSCHEVEDPNAGCRISTLDGRNIAVAVGLMKSKSLDPDFEE 70			
Oy	: : : : : :			
Oy	60 LGTPATSLMDRLQL 75			
Db	71 MESPAKNVENVRAL 86			
RESULT	11			
ZEP1_HUMAN	STANDARD:	PRT:	217 AA.	
ZEP1_HUMAN	01-APR-1990 (rel. 14)			
Dt	01-APR-1990 (rel. 14)			Created)
Dt	01-APR-1990 (rel. 14)			Last sequence update)
Dt	16-OCT-2001 (rel. 40)			Last annotation update)
Dt	Zinc finger protein 40 (human immunodeficiency virus type I enhancer-			
Dt	binding protein 1) (HRV-EF1) [Major histocompatibility complex binding			
Dt	protein 1] (MBP-1) (Positive regulatory domain II binding factor 1)			

DE (PRO11-BE1).  
OS Homo sapiens (human).  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NCBI\_TaxID=9606;  
LN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90169514; PubMed=2106471;  
FA Fan C.M., Maniatis T.;  
RT A DNA-binding protein containing two widely separated zinc finger motifs that recognize the same DNA sequence.  
RN Biochemistry 29:429-434(1990).  
[2]  
RX MEDLINE=91064333; PubMed=2248949;  
FA Omichinski J.G., Clore G.M., Appella E., Sakaiguchi K., Gronenborn A.M.;  
RT High-resolution three-dimensional structure of a single zinc finger protein bound to a DNA double helix.  
RN Biochemistry 29:9324-9334(1990).  
[3]  
RX MEDLINE=92232664; PubMed=1567844;  
FA Omichinski J.G., Clore G.M., Roblen M., Sakaiguchi K., Appella E., Gronenborn A.M.;  
RT High-resolution solution structure of the double Cys2His2 zinc finger protein bound to a DNA double helix.  
RN Biochemistry 31:1307-1317(1992).  
CC -1- FUNCTION: THIS PROTEIN SPECIFICALLY BINDS TO THE DNA SEQUENCE 5'-GGGAGTCCG-3' WHICH IS FOUND IN THE ENHANCER ELEMENTS OF NUMEROUS VIRAL PROMOTERS SUCH AS THOSE OF SV40, CMV, OR HTLV. IN ADDITION, RELATED SEQUENCES ARE FOUND IN THE ENHANCER ELEMENTS OF A NUMBER OF CELLULAR PROMOTERS, INCLUDING THOSE OF THE CLASS I IN T-CELL ACTIVATION.  
CC -1- SUBCELLULAR LOCATION: Nuclear.  
CC -1- INDUCTION: BY MITOGEN AND PHORBOL ESTER.  
CC -1- DOMAIN: CONTAINS TWO SETS OF 2 ZINC-FINGERS, WHICH ARE WIDELY SEPARATED AND RECOGNIZE THE SAME DNA SEQUENCE. THERE IS A FIFTH ZINC-FINGER IN-BETWEEN.  
CC -1- SIMILARITY: STRONG, TO HIVER2.  
CC -1- SIMILARITY: STRONG, TO HIVER2.  
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CC EMBL; X51435; CNA35798.1; -  
DR EMBL; A34203; A34203.  
DR PDB; 3ZNF; 15-JAN-92.  
DR PDB; 4ZNF; 15-JAN-92.  
DR PDB; 1BBO; 31-OCT-93.  
DR TRANSPFC; T00497; -  
DR MIM; 384540; P000822; 2NF-C2H2.  
DR PIRfam; P00096; 2F-C2H2; 5.  
DR PRINTS; P00048; ZINTEFINGER.  
DR SMART; SM00355; 2NF-C2H2; 4.  
DR PROSITE; PS00281; ZINC\_FINGER\_C2H2\_1; 4.  
DR PROSITE; PS01077; ZINC\_FINGER\_C2H2\_2; 4.  
NM Transcription regulation; 3rd-finger; Metal-binding; DNA-binding;  
KV Nuclear protein; Repeat; 3D-structure;  
KW Zinc-finger; Zinc-finger; Zinc-finger; Zinc-finger; Zinc-finger;  
FT ZN\_FING 406 428  
FT ZN\_FING 434 456  
FT ZN\_FING 460 482  
FT ZN\_FING 488 510  
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FT ZN\_FING 544 566  
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FT ZN\_FING

Query Match  
Best Local Similarity 13.1%; Score 74.5; DB 1; Length 2717;  
Matches 28; Conservative 5; Mismatches 23; Indels 17; Gaps 3;

0Y 17 PLSMDLPERSRASKT-----RVHNRCKLMAIGHFGKSLSPSPGLGAFHSLRD 70  
1144 PMSFKEPPERSAPVSFELNFRNGSSLSIKVIG-----ISOESHSPRDSGSHR----- 1193  
DB 71 ORLSHDLICLL 83  
DB 1194 -QALSDALRDEL 1205

## RESULT 12

LITL\_PRTSA STANDARD; PRT: 90 AA.

AD PLSMDLPERSRASKT-----RVHNRCKLMAIGHFGKSLSPSPGLGAFHSLRD 70  
DT 01-NOV-1988 (Rel. 09, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DE 01-MAR-2002 (Rel. 41, Last annotation update)  
OS Phyllomedusa sauvagii (Sauvage's leaf frog),  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Phylomedusa; Anura; Neobatrachia; Bufonidae;  
NCBI\_Taxid=8395;  
RN (1)  
RX SEQUENCE FROM N.A.  
RA MEDLINE=5089778; PubMed=7997236;  
RA Nagalla S.R., Barry B.J., Spindel E.R.;  
RA "Phyllomedusa sauvagii" (Sauvage's leaf frog), the amphibian bombesin-like  
RA peptides Phag 1 and Phag 2 are encoded by the phyllomedusa gene;  
RA potential role of U to C RNA editing in generating neuropeptide  
RT diversity.";  
RL Mol. Endocrinol. 8:943-951(1994).  
RN (2)  
RN SEQUENCE OF 49-57.  
RX MEDLINE=6617052; PubMed=3868775;  
RX de Montigny P., Grapamer G.F., Montecucchi P.C.,  
RX "Phyllomedusa skin: a huge factory and store-house of a variety of  
RT active peptides.";  
RT Peptides 6 Suppl. 3:7-12(1985).  
RL -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: BELONGS TO THE BOMBESIN/NEURONEDIN/B/ANTENNSIN  
CC FAMILY.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL consortium -  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL: S77208; AB03787.1; -;  
DR InterPro: IPR000874; Bombesin.  
DR Pfam: PF00044; Bombesin; 1.  
DR PROSITE: PS00257; BOMBESIN; 1.  
KM Bombesin family; Amidation; Signal.  
FT SIGNAL 1  
FT SIGNAL 30  
FT SIGNAL POTENTIAL.

Query Match  
Best Local Similarity 12.9%; Score 73.5; DB 1; Length 90;  
Matches 20; Conservative 6; Mismatches 24; Indels 1; Gaps 1;

0Y 3 GSLLHPLALANGVSLDLPERSRASKTIRNSGKALAGHNRKKSLE 53  
DB 14 GFALHLLSTFYLVYCKEETEDSDLSRNVLDG-QVANKSLSMKKKSLE 63

## RESULT 13

PKD1\_HUMAN STANDARD; PRT: 4303 AA.

AC P93027-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DE 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Polycystin precursor (autosomal dominant polycystic kidney disease  
GN protein 1).  
GN PKD1.  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eumammalia; Primates; Catarrhini; Hominoidea; Homo.  
NCBI\_Taxid=9606;  
RN (1)  
RX SEQUENCE FROM N.A.  
RA MEDLINE=95254638; PubMed=7736581;  
RA Glucksmann-Kuls M.A., Teyssie O., Woolf E.A., Bouguet-Leret L.,  
RA Deng D., Albertin G.D., Itlis E., Havens F., Munro C., Casey R.,  
RA Redders S.T., Bork P.C., Poltschmidt M., Moehring C., Kraus B.,  
RA Nowicka U., Leung A.L.S., Frischauf A.-M.;  
RA "Polycystic kidney disease: the complete structure of the PKD1 gene  
RT and its protein.";  
RL Cell 81:289-296(1995).  
RN (2)  
RN SEQUENCE OF 2769-4303 FROM N.A.  
RX MEDLINE=94273192; PubMed=8004675;  
RX Ward C.J., Peral B., Hughes J., Thomas S., Kearney L.,  
RX Maccacarty A.B., Sliane-Stanley J., Buckle V.J., Kearney L.,  
RX Higgins D.R., Ratcliffe P.J., Harris P.C., Roelasma J.H.,  
RX Spruit L.L., Saito J.J., Dauwerse H.G., Peters D.J.M.,  
RX Breuning M.H., Nellist M., Brook-Carter P.T., Maheshwar M.M.,  
RX Cordeiro L., Santos H., Carrai P., Sampson J.R., Jensen B.,  
RX Verhoef S., Lindhout D., Haller D.J.J., and A.R.K., Hansen B.,  
RT "The polycystic kidney disease 1 gene encodes a 14 kb transcript and  
RT lies within a duplicated region on chromosome 16. The European  
RT Polycystic Kidney Disease Consortium.";  
RL Cell 77:881-894(1994).  
RN (3)  
RN SEQUENCE BY NMR OF 276-354  
RX MEDLINE=9910776; PubMed=9889186;  
RX Bycroft M., Bateman A., Clarke J., Hamill S.J., Sandford R.,  
RX Thomas R.L., Chottha C.;  
RT "The structure of a PKD domain from polycystin-1: implications for  
RT polycystic kidney disease.";  
RN EMBL J. 18:297-305(1999).  
RN (4)  
RN VARIANT APPED 3748-ARG->ALA-3753 DEL, AND VARIANT ASP->3632.  
RX MEDLINE=96108969; PubMed=8554072;  
RX Peral B., San Millan J.L., Ong A.C.M., Gamble V., Ward C.J.,  
RX Strong C., Harris P.C.;  
RT "Screening the 3' region of the polycystic kidney disease 1 (PKD1)  
RT gene reveals six novel mutations.";  
RL Am. J. Hum. Genet. 58:86-96(1996).

- [13] VARIANTS ADPKD P-2993; R-3016 AND V-3511, AND VARIANTS M-3510 AND M-3511. PubMed:9195561.
- RA Peral B., Gamble V., Strong C., Ong A.C.M., Sloane-Stanley J., Zierres K., Winearls C.G., Harris P.C., "Identification of mutations in the duplicated region of the polycystic kidney disease 1 gene (PKD1) by a novel approach." Am. J. Hum. Genet. 60:1399-1410(1997).
- RL [14] VARIANT ALA-4058. PubMed:9150733.
- RX MEDLINE-97295091; PubMed:9150733.
- RA Constantiniides R., Xenophonos S.L., Neophytou P., Nomura S., Pterides A., Constantinou-Deltas C.D., "New amino acid polymorphism, AlaVal4058, in exon 45 of the polycystic kidney disease 1 gene: evolution of alleles." Hum. Genet. 99:644-647(1997).
- RP VARIANTS T-2760; P-2761; V-2763; T-2764; Q-2791; T-2826; L-3008 AND L-3064. PubMed:9285784.
- RA MEDLINE-97449169; PubMed:9285784.
- RA Melnick T.J., Plontek K.B., Cordal T.M., Weber H., Gandolph M.A., Qian F., Lena X.M., Neumann H.P.H., Germino G.G., "An unusual pattern of mutations in the duplicated portion of PKD1 is revealed by use of a novel strategy for mutation detection." J. Mol. Genet. 6:1443-1461(1997).
- RP VARIANT ADPKD THR-3678. PubMed:9259200.
- RA MEDLINE-97403939; PubMed:9259200.
- RA Turco A.E., Rossetti S., Bresin E., Englisch S., Corra S., Pignatti P.F., "Three novel mutations of the PKD1 gene in Italian families with autosomal dominant polycystic kidney disease." Hum. Mutat. 10:167-167(1997).
- RP VARIANT ADPKD ASP-4032, AND VARIANT VAL-4045. PubMed:9521593.
- RX MEDLINE-98180892; PubMed:9521593.
- RA Daniells G., Maheshwar M.M., Lazarou L., Davies F., Coles G., Revine D., recurrent mutations in the PKD1 (polycystic kidney disease) gene. Hum. Genet. 102:216-220(1998).
- RP VARIANT ADPKD MET-3375. PubMed:9921908.
- RX MEDLINE-99118881; PubMed:9921908.
- RA Kopolides M., Constantiniides R., Kyriakides G., Hadjilavriel M., Petralias P.C., Pterides A., Deltas C.C., "Identification of mutations in the polycystic kidney disease 1 gene (PKD1) in the family of a patient with a mutation in the PKD1 gene." Hum. Genet. 103:709-717(1998).
- RP VARIANTS ADPKD L-324 AND S-845, AND VARIANTS R-1399 AND L-1786. PubMed:99294580; PubMed:10364515.
- RA Thomas R.L., McConnell R., Whittecker J., Kilpatrick P., Bradley J., Sandford R., "Identification of mutations in the repeated part of the autosomal dominant polycystic kidney disease type 1 gene, PKD1, by long-range PCR." Am. J. Hum. Genet. 65:39-49(1999).
- RL [12] VARIANTS ADPKD P-2392 AND F-2423, AND VARIANTS R-1399; Q-2548 AND R-2638. PubMed:10577909.
- RA MEDLINE-10577909.
- RA Phadokitcharoen B., Johnson A., Gandolph M., Wang M., Bridel G., Kilmer K.W., Kimbrell W., Gadow P., Germino G.G., "Mutation detection of PKD1 identifies a novel mutation common to three families with aneurysms and/or very-early-onset disease." Am. J. Hum. Genet. 65:1561-1571(1999).
- RL [13] VARIANTS ADPKD L-3994--F-3996 DUP1; G-4136 AND C-4154, AND VARIANTS. PubMed:10844157; PubMed:10876501; PubMed:10876501.
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- RA "PCR screening of PKD1 gene reveals novel mutations in a large cohort of 146 unrelated patients." Hum. Genet. 105:231-239(1999).
- RL [14] VARIANTS ADPKD 3748-R-V-3752 DEL AND L-4132 DEL, AND VARIANT V-4045. PubMed:10112427; PubMed:10647901.
- RX MEDLINE-10112427; PubMed:10647901.
- RA Afzal A.R., Hand M., Ternes-Percelle E., Saggart-Malik A., Taylor R., Jeffrey S., "Novel mutations in the 3' region of the polycystic kidney disease 1 gene (PKD1) gene." Hum. Genet. 105:648-653(1999).
- RL [15] VARIANTS ADPKD PRO-4225 AND TRP-4276. PubMed:10922041; PubMed:10922041.
- RX MEDLINE-99217041; PubMed:10922041.
- RA Badenes C., Torra R., San Millan J.L., Lucero L., Mula M., Estivill X., Darnell A., "Mutational analysis within the 3' region of the PKD1 gene." Kidney Int. 55:1225-1233(1999).
- RL [16] VARIANTS ADPKD MET-2550 AND TRP-2339, AND VARIANTS CYS-2379; LEU-3066; VAL-3119 AND LEU-3193. PubMed:10854095.
- RX MEDLINE-10311156; PubMed:10854095.
- RA Pericchio R., Mercier B., Quee I., Carre A., Simon P., Whebe B., Cledes J., Ferec C., "Novel mutations in the duplicated region of PKD1 gene." Eur. J. Hum. Genet. 8:353-359(2000).
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- RX MEDLINE-10382887; PubMed:10923040.
- RA Kopolides M., Mean R., Demettrio K., Constantiniides R., Pterides A., Harris P.C., Deltas C.C., "Screening of the PKD1 duplicated region reveals multiple single nucleotide polymorphisms and a de novo mutation in Hellenic polycystic kidney disease families." Mutat. 16:178-178(2000).
- RP VARIANTS ADPKD GLN-3719 AND PRO-3852, AND VARIANT VAL-4045. PubMed:10514565; PubMed:10514565.
- RX MEDLINE-10514565; PubMed:10514565.
- RA Agueri G., Savelli S., Garbo M., Bozza A., Angello G., Penolazzi L., De Poli Vitali B., La Torre G., Cappelli G., Piva R., del Senno L., "Novel splicing and missense mutations in autosomal dominant polycystic kidney disease 1 (PKD1) gene: expression of mutated PKD1 protein." Hum. Mutat. 16:444-445(2000).
- RL [19] VARIANTS ADPKD SER-1166; GLU-1956; CYS-2408 AND GLY-2442--2443 INS, AND VARIANTS HIS-1995 AND ASN-2604. PubMed:1067506; PubMed:11012875.
- RX MEDLINE-1067506; PubMed:11012875.
- RA Phadokitcharoen B., Whittecker J., Ahn C., Whang D.-Y., Burkhardt B., "Thirteen novel mutations of the replicated region of PKD1 in an Asian population." Kidney Int. 58:1400-1412(2000).
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- RA Haeng D.-Y., Lee J.-G., Noh J.-H., Lee C.-Y., Lee C.-Y., "Novel mutations of the PKD1 gene in Korean patients with autosomal dominant polycystic kidney disease." Mutat. Res. 433:39-45(2000).
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- RX MEDLINE-11063179; PubMed:11113377.
- RA Rossetti S., Strieckl E., Gamble V., Burton S., Sneddon V., Peral B., Roy S., Bakaloglu A., Komel R., Winearls C.G., Harris P.C., "Mutation analysis of the entire PKD1 gene: genetic and diagnostic implications." Am. J. Hum. Genet. 68:46-63(2001).
- RL [22] VARIANTS ADPKD P-2993; R-3016 AND V-3511, AND VARIANTS M-3510 AND M-3511. PubMed:9195561.





